

Comparison of Mouse and Human TNF Family Related Proteins (TFRPs)

1	human	MSLLDFEISA	RRLPLPRSLG	SRDGGAVRQA	OPPAPMAARR	SQRRRGRGE	50
	mouse
51	human	PGTALLVPLA	<u>LGLGLALACL</u>	<u>GLLLAVVSLG</u>	<u>SRASLSAQEP</u>	<u>AQEELVAEED</u>	100
	mouseV	<u>LSIIGLALACL</u>	<u>GLLLVvvSLG</u>	<u>SWATLSAQEP</u>	<u>SQEELTAEDR</u>	1/8
101	human	QDPSELNPQT	EESQDPAPFL	NRLVVRPRRSA	PKGRKTRARR	<u>AIAAHYEVHP</u>	150
	mouse	REPPELNPQT	EESQDVVPFL	EQLVVRPRRSA	PKGWMKARP RR	<u>AIAAHYEVHP</u>	
151	human	RPGQDGAAQAG	VDGTVSGWEE	ARIINSSSSPLR	YNRQIGEFTIV	TRAGLYYYLYC	200
	mouse	RPGQDGAAQAG	VDGTVSGWEE	TKINNSSSPLR	YDRQIGELTV	<u>TRAGLYYYLYC</u>	
201	human	QVHFDEGKAV	YLKLDLLVDG	VIALRCLEEF	SATAASSSLGP	QLRLCQVSGL	250
	mouse	QVHFDEGKAV	YLKLDLLVNG	VIALRCLEEF	SATAASSSPGP	QLRLCQVSGL	
251	human	LALRPGSSLR	IRTLPLWAHLK	AAPFLTYFGL	FQVH	284	
	mouse	LPLRPGSSLR	IRTLPLWAHLK	AAPFLTYFGL	FQVH		

FIG. 1

Sequence Comparison of Human Ligands in the TNF Family

An alignment of 10 human members of the TNF ligand family illustrating the variations in the length of the intracellular N-terminal domains and the stalk regions spacing the C-terminal receptor binding domain from the transmembrane region (beginning just before the first beta strand). The N terminus of human FasL has been truncated. The alignment weighs cysteine conservation heavily and due to the very poor homology in certain regions between some family members, many alternative alignments can be proposed varying in the details. The bars over the sequences indicate beta strand structures in TNF and LT with the nomenclature being that used by Eck and Sprang. Canonical N-linked glycosylation sites are underlined as are probable transmembrane sequences and the disulfide linked cysteines in TNF are marked with dots. Starred sequences are motifs useful in the recognition of TNF family members.

A

hTNP SSPLAQAVRSSSRTP-----
hLT-α -----
hLT-β QGLGFQKLPEEEPEETDLS-----
hFasL MHTASSELEKQIGHPSPPPEKK-----
hTPRP DQDPSELNPQTEESQDPAPFLNRLVRPRSAPKGRKTA-----
hTPA1L PLKEDDSYWDPNDEESMNSPCWQVKWQLRQLVRKMLRTSEETI1STVQEKQONISPLYRGPQRVAAHITGTRGRSNLTSSPNSKNEKALGRKINSWE-----
hCD27L -----
hCD30L NCSEDULCILKRAFP-----
hCD40L FMKTIQRCNTGERSLSLLNCEEIKSQFEGFVKD1M1NKEETKKENSFEMQKGQ-----
h4-1BBL PRLEGPPELSPDDPAGLIDLRQGM-----
* * * * *

A'

hTNP SDKPVAHVVANPQAEGQ-----
hLT-α TLKPAAHLLIGDPSK-QNS-----
hLT-β PGLPAAHLLIGAPLKGOG-----
hFASL ELRKVAHLLTGKNSRSMP-----
hTPRP RRAIAAHYEVHPRPGQDGAQAGVGDGT-----
hTPA1L LYWQCC-----
hCD27L LSWNKD-----
hCD30L LQWAEK-----
hCD40L LSWYSD-----
* * * * *

B

hTNP -----
hLT-α -----
hLT-β -----
hFASL -----
hTPRP -----
hTPA1L -----
hCD27L -----
hCD30L -----
hCD40L -----
h4-1BBL -----
* * * * *

B'

hTNP -----
hLT-α -----
hLT-β -----
hFASL -----
hTPRP -----
hTPA1L -----
hCD27L -----
hCD30L -----
hCD40L -----
h4-1BBL -----
* * * * *

C

hTNP RANALLAN-GVELRD--NQ-LVVPSEGLYLIX-SQVLFKGQGCPSTHVLILHTTISRLAVS-----
hLT-α TDRAPFLQD-GFSLs--NNs-LLVPTSGIYFVINSQVVTSGKAY-SPKAT-SPLYLAHEVQLFSSQYPHPV--LLSSQRM---VY-PGLQE-----
hLT-β KEQAFLT-SGTQPSDAEG--LALPQDGCLLYLTCLVGYZRGRAPPGGDPQQRSTVLRSLLYRAGAYGPGTPELLEGAETVTPVLDPARRGYG-----
hFASL YGIVLl--SGVKYTK-GG--LVTINETGLYFVY-SKVYPRGQSCNNQPLSHKTYMRN---SK---YPQDL--VMEGKm--MSY--CTTGQ-----
hTPRP R1N5SPLRYNRQI--GE--P1VTRAGLYLY-CQVXHDFEGKAVYLKLDLIVDGVLALRCLEEFSATAASSLGQPLRL-----CQVSGLL-----
hTPA1L RSGHSPLSNLHLRN--GE--LVIHEKGFYIY-SOTYPRQEELKENTKNDKQMVQYIYKTS---YPDPI--LLMKSA1NS---CWSKDAEY-----
hCD27L PALGRSPFLXGPEL-DKGQ--LRIHRDG1YMH1-QVTLAI--CSSTTASRHPTTLAVGICSPASRSIS---L1RLSPFHQG---CTIV-----
hCD30L G---ILHGVRYQD-GN--LVIQFPGLYFII-CQLQFLVQ-CPNNSVDLKLELLINKH1K--QALVT---VCESGMQTKHVYQNLSQL-----
hCD40L GYTMSNNLVTL--ENGKQ-LTVKRGQGLYIY-A-QVTP---CSNREASSQAFPLAS1CLKSPGFRERI---LLRAAN-THSSAKPCGQOSIH-----
h4-1BBL DGAGSSYLSQGLRYEEDKKELWVDSPGLYYYVFLLEKLSPFTNTGKVKVQGWVSLVQAKP--QVDDDFDN---LAL---TVELP-PCSMENKLVDRS-----
* * * * *

D

hTNP -----
hLT-α -----
hLT-β -----
hFASL -----
hTPRP -----
hTPA1L -----
hCD27L -----
hCD30L -----
hCD40L -----
h4-1BBL -----
* * * * *

E

hTNP -----
hLT-α -----
hLT-β -----
hFASL -----
hTPRP -----
hTPA1L -----
hCD27L -----
hCD30L -----
hCD40L -----
h4-1BBL -----
* * * * *

F

hTNP P-WYEPIYLGGVFQLEKGDRLSAETINRPOYLDFAESGQ---VYFGJIAL-----
hLT-α P-WLHSMTYHGAFAFQLTQDQLSTHTD1PHLVL--SPS--TVFFGAFAFAL-----
hLT-β PLWYTSVGFGGVLVQLRGERVYVNLISHPDMDFAR--GKT-FFGAVMVG-----
hFASL -MWARSSYLGAVFNNTSADHLYVNVSEL--SLVNFEESQT-FFGLYKL-----
hTPRP ALRPGSSLR1R1LTPWAHLKAAPFL-----T-YFGLFQVH-----
hTPA1L --GLYSIYQGGIFELKENDRIFVSVTNEHLDMDHEA---S-FFGAFLVG-----
hCD27L -SQR1TPLARGDTLC1NLTG1TLLPSR-NTDE-----T-FFGVQWVRP-----
hCD30L --LDYLQVNT1S1SVN1VDTFQY1DTST-FPLE-NVL-----S-IFLYSNSD-----
hCD40L --LGGVFELQPGASVFVNNTDPSQVSHG---TGFTS-FGLLKL-----
h4-1BBL --WSQULLKAGHRLSVGLRAYLHGAQDAYRDWELSYPPNTS-FGLFLVKPDDNPWE-----

G

hTNP -----
hLT-α -----
hLT-β -----
hFASL -----
hTPRP -----
hTPA1L -----
hCD27L -----
hCD30L -----
hCD40L -----
h4-1BBL -----
* * * * *

H

hTNP -----
hLT-α -----
hLT-β -----
hFASL -----
hTPRP -----
hTPA1L -----
hCD27L -----
hCD30L -----
hCD40L -----
h4-1BBL -----
* * * * *

FIG. 2B

APPROV'D	BY	FIG.
BY	17	ASS SUBCLASS
DRAFTSMAN		

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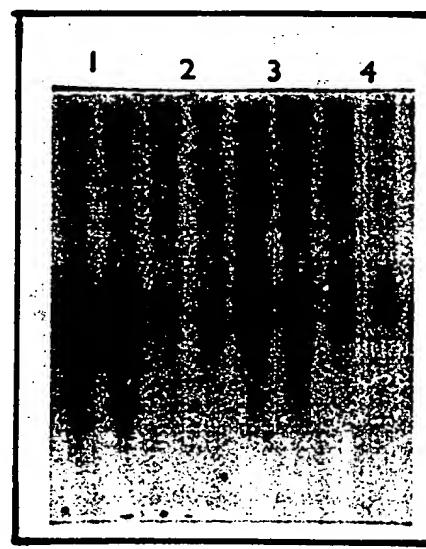


FIG. 3

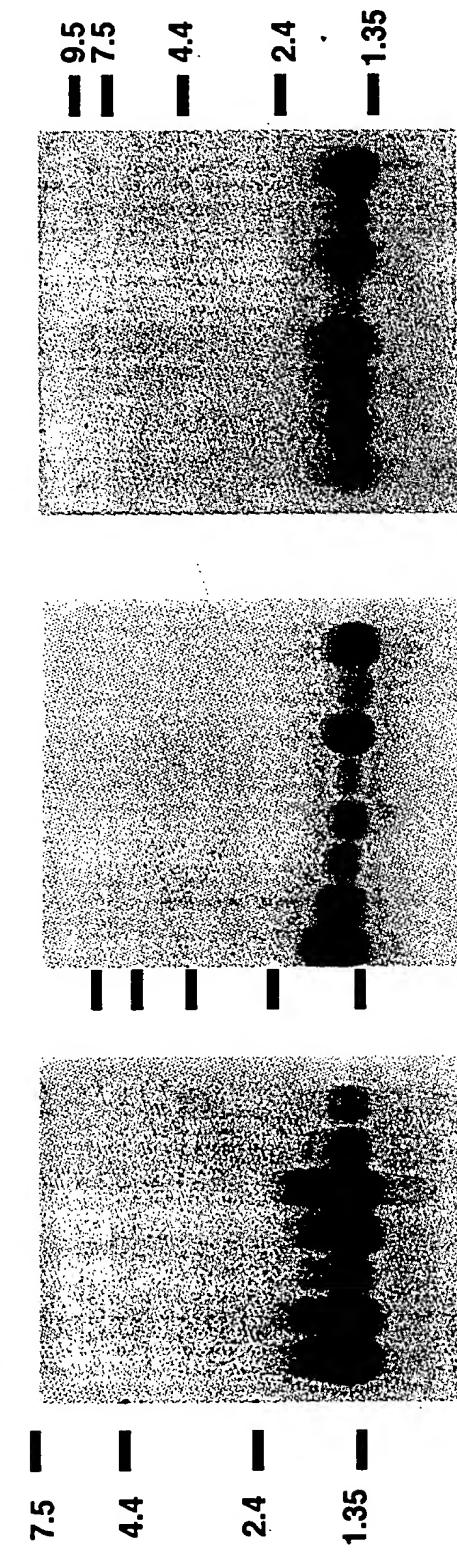
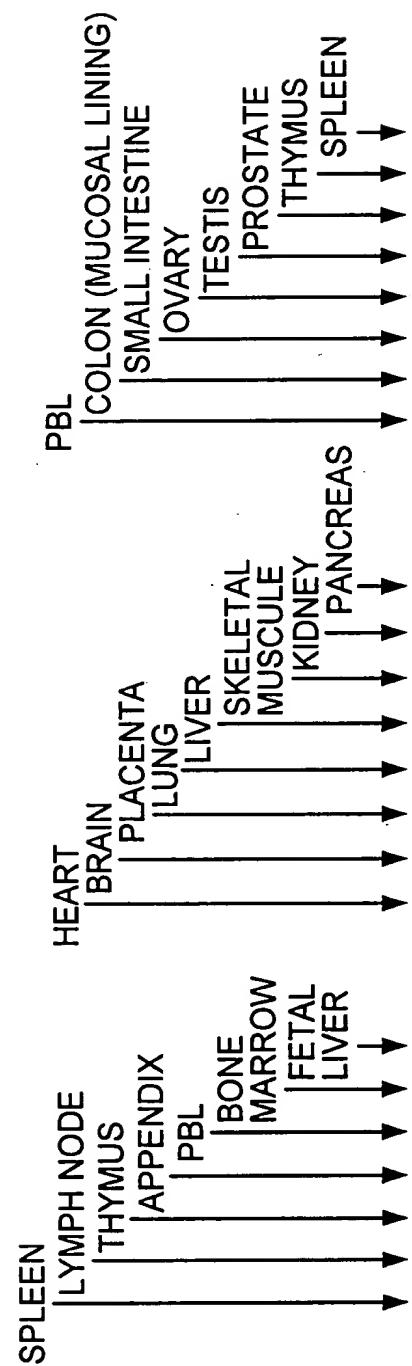


FIG. 4

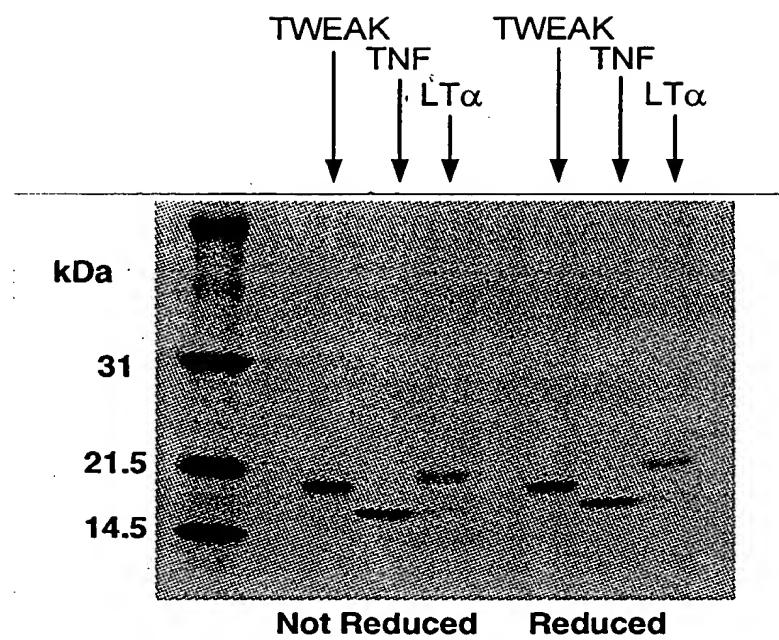


FIG. 5

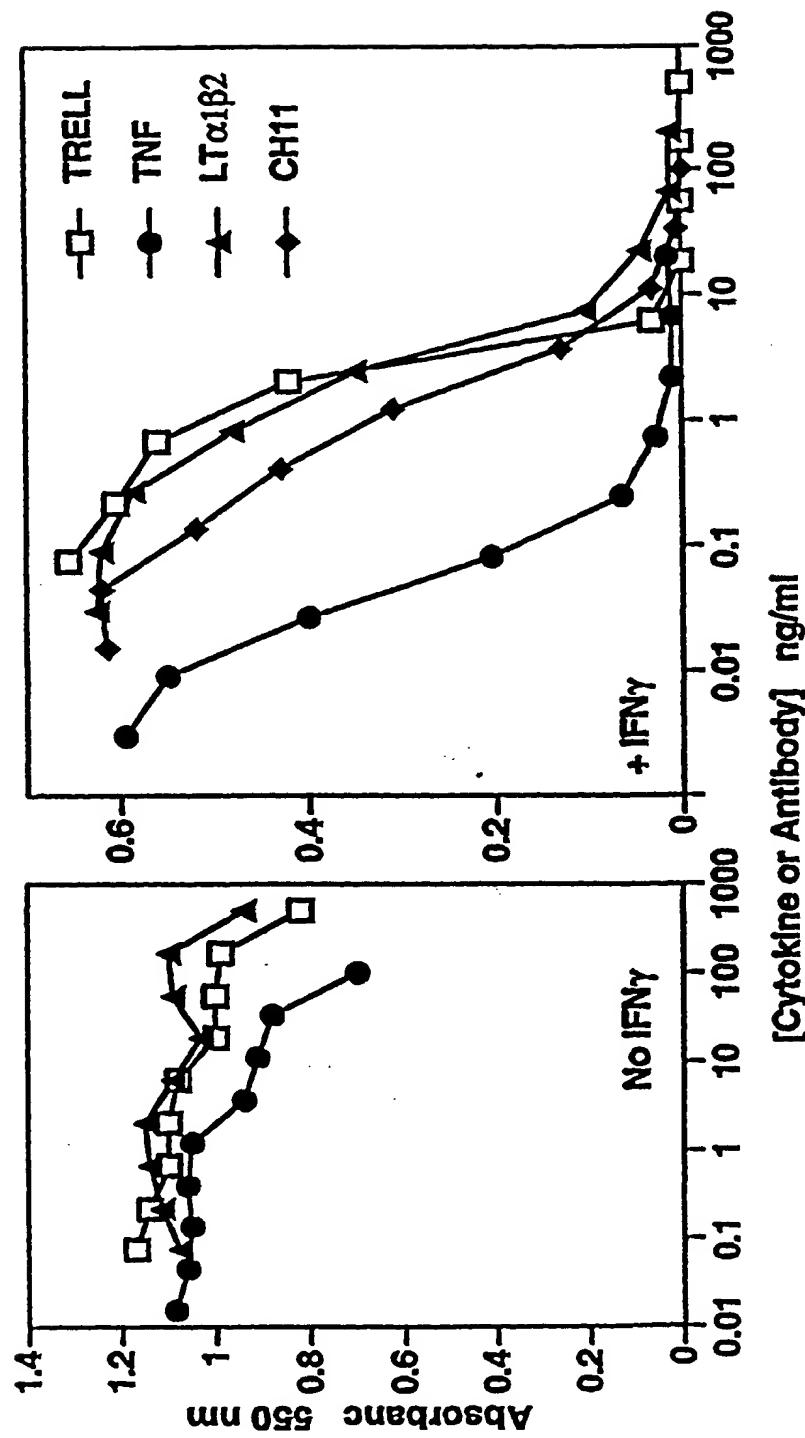


FIG. 6A

APPROVED	BY	FIG.
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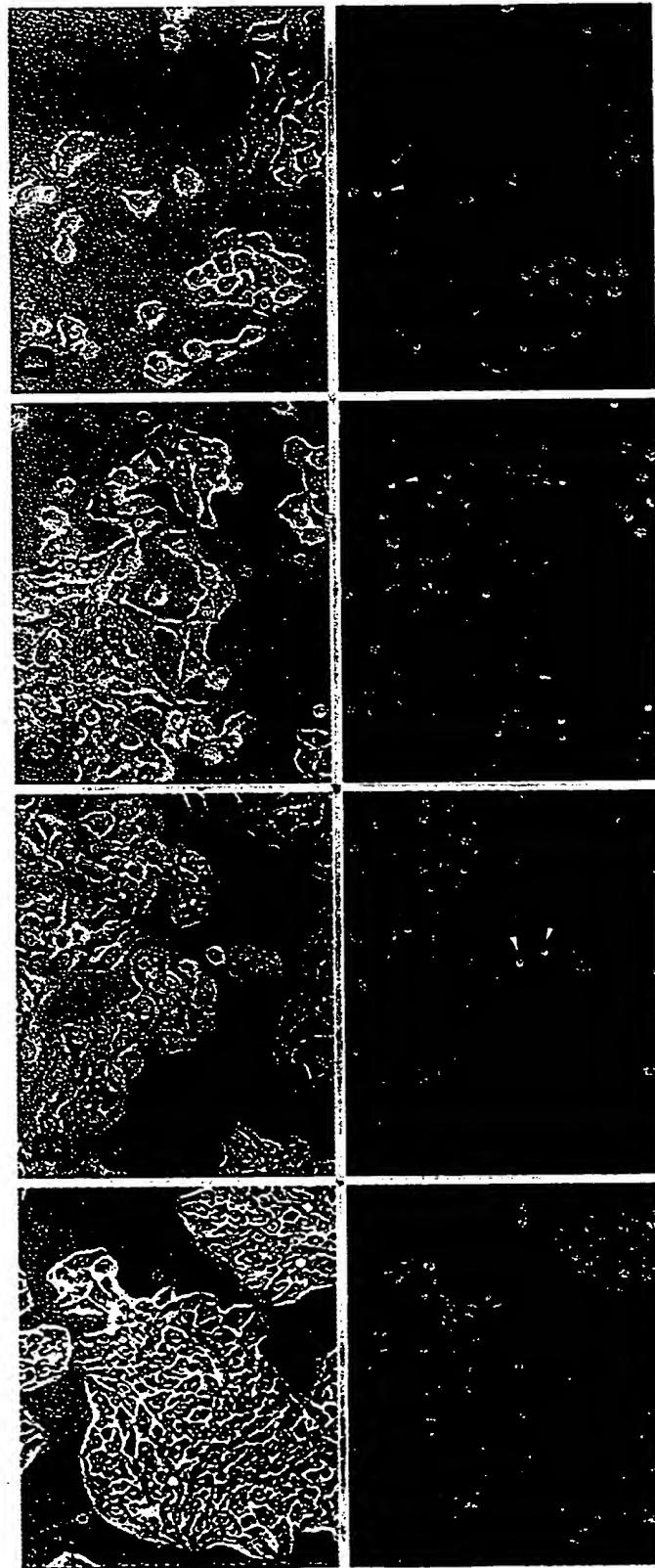


FIG. 6B